

TFS

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/720,934

DATE: 11/14/2001
TIME: 14:05:23

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF3\11142001\I720934.raw

3 <110> APPLICANT: Korenberg, Julie R
4 Chen, Xiao-Ning
6 <120> TITLE OF INVENTION: ISOLATED SH3 GENES ASSOCIATED WITH MYELOPROLIFERATIVE
7 DISORDERS AND LEUKEMIA, AND USES THEREOF
9 <130> FILE REFERENCE: 2320-1-001PCT
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/720,934 *✓*
C--> 12 <141> CURRENT FILING DATE: 2001-10-03
14 <150> PRIOR APPLICATION NUMBER: 60/082,007
15 <151> PRIOR FILING DATE: 1998-04-16
17 <160> NUMBER OF SEQ ID NOS: 109
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 5199
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
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29 gtgagcggca ctgatttgc cctggggcgg cagcgcggac ccgccccggag atgaggcgctc 180
30 gattagcaag gtaaaagtaa cagaaccatg gtcagttc caacaccttt tgggtggcagc 240
31 ctggatatct gggccataac ttttagagggaa agagcgaagc atgatcagca gttccatagt 300
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67 cttaaccattt ctgcacagga aaatgtaaaa gtggtgtatt accgggact gtacccttt 2460
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107 ttaaacacta gttggaagct ctcataaaa atgcctgctg ctcacagcac agaaaatggg 4860
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116 <211> LENGTH: 1143
117 <212> TYPE: PRT
118 <213> ORGANISM: Homo sapiens
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125 20 25 30
127 Lys Pro Ile Ser Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe
128 35 40 45
130 Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu
131 50 55 60
133 Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile
134 65 70 75 80
136 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser
137 85 90 95
139 Ala Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala
140 100 105 110
142 Pro Ala Phe Gly Met Gly Gly Ile Ala Ser Met Pro Pro Leu Thr Ala
143 115 120 125
145 Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro
146 130 135 140
148 Thr Leu Val Ser Ser Val Pro Thr Ala Ala Val Pro Pro Leu Ala Asn
149 145 150 155 160
151 Gly Ala Pro Pro Val Ile Gln Pro Leu Pro Ala Phe Ala His Pro Ala
152 165 170 175
154 Ala Thr Leu Pro Lys Ser Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser
155 180 185 190
157 Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser
158 195 200 205
160 Val Pro Pro Val Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys
161 210 215 220
163 Tyr Arg Gln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu
164 225 230 235 240
166 Thr Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln
167 245 250 255
169 Ala Gln Leu Ala Ser Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly
170 260 265 270
172 Lys Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val
173 275 280 285
175 Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile

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179	305	310	315
181	Ser Ser Thr Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Val Leu Glu		
182	325	330	335
184	Asp Glu Gln Gln Gln Leu Glu Lys Lys Leu Pro Val Thr Phe Glu Asp		
185	340	345	350
187	Lys Lys Arg Glu Asn Phe Glu Arg Gly Asn Leu Glu Leu Glu Lys Arg		
188	355	360	365
190	Arg Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala		
191	370	375	380
193	Gln Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu		
194	385	390	395
196	Gln Glu Arg Lys Arg Gln Leu Glu Leu Glu Lys Gln Leu Glu Lys Gln		
197	405	410	415
199	Arg Glu Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu		
200	420	425	430
202	Arg Arg Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu		
203	435	440	445
205	Trp Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu		
206	450	455	460
208	Gln Glu Asp Ile Val Val Leu Lys Ala Lys Lys Lys Thr Leu Glu Phe		
209	465	470	475
211	Glu Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu		
212	485	490	495
214	Gln Asp Ile Arg Cys Arg Leu Thr Thr Gln Arg Gln Glu Ile Glu Ser		
215	500	505	510
217	Thr Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln		
218	515	520	525
220	Gln Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu		
221	530	535	540
223	Lys Gln Ile Leu Asn Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu		
224	545	550	555
226	His Arg Asp Ser Leu Val Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu		
227	565	570	575
229	Leu Ala Arg Gln His Leu Arg Asp Gln Leu Asp Glu Val Glu Lys Glu		
230	580	585	590
232	Thr Arg Ser Lys Leu Gln Glu Ile Asp Ile Phe Asn Asn Gln Leu Lys		
233	595	600	605
235	Glu Leu Arg Glu Ile His Asn Lys Gln Gln Leu Gln Lys Gln Lys Ser		
236	610	615	620
238	Met Glu Ala Glu Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ile Ile		
239	625	630	635
241	Glu Leu Glu Lys Gln Lys Glu Glu Ala Gln Arg Arg Ala Gln Glu Arg		
242	645	650	655
244	Asp Lys Gln Trp Leu Glu His Val Gln Gln Glu Asp Glu His Gln Arg		
245	660	665	670
247	Pro Arg Lys Leu His Glu Glu Lys Leu Lys Arg Glu Glu Ser Val		
248	675	680	685

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250 Lys Lys Lys Asp Gly Glu Glu Lys Gly Lys Gln Glu Ala Gln Asp Lys
251 690 695 700
253 Leu Gly Arg Leu Phe His Gln His Gln Glu Pro Ala Lys Pro Ala Val
254 705 710 715 720
256 Gln Ala Pro Trp Ser Thr Ala Glu Lys Gly Pro Leu Thr Ile Ser Ala
257 725 730 735
259 Gln Glu Asn Val Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu
260 740 745 750
262 Ser Arg Ser His Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met
263 755 760 765
265 Val Asp Glu Ser Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu
266 770 775 780
268 Lys Gly Lys Thr Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile Pro
269 785 790 795 800
271 Glu Asn Glu Val Pro Ala Pro Val Lys Pro Val Thr Asp Ser Thr Ser
272 805 810 815
274 Ala Pro Ala Pro Lys Leu Ala Leu Arg Glu Thr Pro Ala Pro Leu Ala
275 820 825 830
277 Val Thr Ser Ser Glu Pro Ser Thr Thr Pro Asn Asn Trp Ala Asp Phe
278 835 840 845
280 Ser Ser Thr Trp Pro Thr Ser Thr Asn Glu Lys Pro Glu Thr Asp Asn
281 850 855 860
283 Trp Asp Ala Trp Ala Ala Gln Pro Ser Leu Thr Val Pro Ser Ala Gly
284 865 870 875 880
286 Gln Leu Arg Gln Arg Ser Ala Phe Thr Pro Ala Thr Ala Thr Gly Ser
287 885 890 895
289 Ser Pro Ser Pro Val Leu Gly Gln Gly Glu Lys Val Glu Gly Leu Gln
290 900 905 910
292 Ala Gln Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp Asn His Leu Asn
293 915 920 925
295 Phe Asn Lys Asn Asp Val Ile Thr Val Leu Glu Gln Gln Asp Met Trp
296 930 935 940
298 Trp Phe Gly Glu Val Gln Gly Gln Lys Gly Trp Phe Pro Lys Ser Tyr
299 945 950 955 960
301 Val Lys Leu Ile Ser Gly Pro Ile Arg Lys Ser Thr Ser Met Asp Ser
302 965 970 975
304 Gly Ser Ser Glu Ser Pro Ala Ser Leu Lys Arg Val Ala Ser Pro Ala
305 980 985 990
307 Ala Lys Pro Val Val Ser Gly Glu Glu Ile Ala Gln Val Ile Ala Ser
308 995 1000 1005
310 Tyr Thr Ala Thr Gly Pro Glu Gln Leu Thr Leu Ala Pro Gly Gln Leu
311 1010 1015 1020
313 Ile Leu Ile Arg Lys Lys Asn Pro Gly Gly Trp Trp Glu Gly Glu Leu
314 1025 1030 1035 1040
316 Gln Ala Arg Gly Lys Lys Arg Gln Ile Gly Trp Phe Pro Ala Asn Tyr
317 1045 1050 1055
319 Val Lys Leu Leu Ser Pro Gly Thr Ser Lys Ile Thr Pro Thr Glu Pro
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322 Pro Lys Ser Thr Ala Leu Ala Ala Val Cys Gln Val Ile Gly Met Tyr

VERIFICATION SUMMARY
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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date